

Figure 1A

1	TAGTTCTAGATCGCGAGCGGCGCCGGCGGGCCCCGAGGAGGGAGGAAGGAAGGAAGGAAGG	60
61	CTGGAAGGAAGGAAGCCAGGAAAGAAAGAAGGAAAGAAAGGAAGGCAAGAAGGAAGGCGG	120
121	GCGGCGGGCGAGGGCGCGGGGCCGGACGGCAGGCGGGCGCGAGGCGAGGAGGCAGAGCGG	180
181	CCCCCCCAGCCCCACCGCCGCGCTGCGGAAGCCCCCTCCCCACCCAGGAGCCGGGGAGG	240
241	GGGAGAGCGCGAGAGGCTCCAGGCCCCGGCCGAGCCCCGCCCCCGCGCCTCCCCGCGAG	300
301	CGGGCCTTGACCCCCAAATTCCTGAGCCTCATTGGGGGGGTCTCCCCCACGGGCGGGG	360
361	CATGCTGCCCCCGGAAGGAACCCCTCTCCTCGCTCACGATCTCGACAGGAAGCCCTGGA	420
421	GAAGTGGGGAGGCAGAGACCCCGCTGGCCGGAGGCATGTGGAGGGGGGGCGCTGGGCGC	480
481	AGGGAGAGGCCAGCGGAAGCCAAGCCACCAGGCCCCCAGCGTCCACGCGGAGCATGAA	540
541	CATTGAGGATGGCGCGTGCCCGGGCTCCCCGTGCCCCCGCTGCCGCCCCGGTAGGATGT	600
1	<u>M A R A R G S P C P P L P P G R M S</u>	18
601	CCTGGCCCCACGGGGCATTGCTCTTCTCTGGCTCTTCTCCCCACCCCTGGGGGCCGGTG	660
19	<u>W P H G A L L F L W L F S P P L G A G G</u>	38
661	GAGGTGGAGTGGCCGTGACGTCTGCCGCCGGAGGGGGCTCCCCGCCGGCCACCTCCTGCC	720
39	G G V A V T S A A G G G S P P A T S C P	58
721	CCGTGGCCTGCTCCTGCAGCAACCAGGCCAGCCGGGTGATCTGCACACGGAGAGACCTGG	780
59	V A C S C S N Q A S R V I C T R R D L A	78
781	CCGAGGTCCCAGCCAGCATCCCGGTCAACACGCGGTACCTGAACCTGCAAGAGAACGGCA	840
79	E V P A S I P V N T R Y L N Q E N G I	98
841	TCCAGGTGATCCGGACGGACACGTTCAAGCACCTGCGGCACCTGGAGATTCTGCAGCTGA	900
99	Q V I R T D T F K H L R H L E I Q L S	118
901	GCAAGAACCTGGTGCGCAAGATCGAGGTGGGCGCCTTCAACGGGCTGCCAGCCTCAACA	960
119	K N L V R K I E V G A F N G L P S L N T	138
961	CGCTGGAGCTTTTTGACAACCGGCTGACCACGGTGCCACGCAGGCCTTCGAGTACCTGT	1020
139	L E L F D N R L T T V P T Q A F E Y L S	158

1021	CCAAGCTGCGGGAGCTCTGGCTGCGGAACAACCCCATCGAGAGCATCCCCTCCTACGCCT	1080
159	K ²³ ₁₄ R E <u>L</u> W ⁴⁴ ₁₄ R N N P I E S I P S Y A F	178
1081	TCAACCGCGTGCCCTCGCTGCGGCGCCTGGACCTGGGCGAGCTCAAGCGGCTGGAATACA	1140
179	N R V P S ¹¹¹ ₁₄ R R ¹¹² ₁₄ D ¹¹³ ₁₄ G E L K R <u>L</u> E Y I	198
1141	TCTCGGAGGCGGCCTTCGAGGGGCTGGTCAACCTGCGCTACCTCAACCTGGGCATGTGCA	1200
199	S E A A F E G <u>L</u> V N ¹²⁶ ₁₄ R Y ¹²⁷ ₁₄ N ¹²⁸ ₁₄ G M C N	218
1201	ACCTCAAGGACATCCCCAACCTGACGGCCCTGGTGCGCCTGGAGGAGCTGGAGCTGTTCGG	1260
219	<u>L</u> K D I P N <u>L</u> T A <u>L</u> V R ²²⁶ ₁₄ E E <u>L</u> E ²²⁷ ₁₄ S G	238
1261	GCAACCGGCTGGACCTGATCCGCGCGGGCTCCTTCCAGGGTCTCACCAGCCTGCGCAAGC	1320
239	N R <u>L</u> D L I R P G S F Q G ²⁴⁶ ₁₄ T S <u>L</u> R K ²⁴⁷ ₁₄	258
1321	TGTGGCTCATGCACGCCAGGTAGCCACCATCGAGCGCAACGCCTTCGACGACCTCAAGT	1380
259	W <u>L</u> M H A Q V A T I E R N A F D D <u>L</u> K S	278
1381	CGCTGGAGGAGCTCAACCTGTCCCACAACAACCTGATGTGCTGCCCCACGACCTCTTCA	1440
279	<u>L</u> E E L N L S H N N ²⁸⁶ ₁₄ M S <u>L</u> P H D <u>L</u> F T	298
1441	CGCCCCGTCACCGCCTCGAGCGCGTGACCTCAACCACAACCCCTGGCATTGCAACTGCG	1500
299	P <u>L</u> H R <u>L</u> E R V H ³⁰⁶ ₁₄ N H N P W H C N C D	318
1501	ACGTGCTCTGGCTGAGCTGGTGGCTCAAGGAGACGGTGCCAGCAACACGACGTGCTGCG	1560
319	V L W <u>L</u> S W W L K E T V P S N T T C C A	338
1561	CCCGCTGTCTATGCGCCCGCCGGCCTCAAGGGGCGCTACATTGGGGAGCTGGACCAGTCGC	1620
339	R C H A P A G ³⁴⁶ ₁₄ K G R Y I G E L D Q S H	358
1621	ATTTACCTGCTATGCGCCCGTCATCGTGGAGCCGCCCACGGACCTCAACGTCACCGAGG	1680
359	F T C Y A P V I V E P P T D L N V T E G	378
1681	GCATGGCTGCCGAGCTCAAATGCCGCACGGGCACCTCCATGACCTCCGTCAACTGGCTGA	1740
379	M A A E L K C R T G T S M T S V N W L T	398
1741	CGCCCAACGGCACCCCTCATGACCCACGGCTCCTACCGCGTGCGCATCTCCGTCTGCATG	1800
399	P N G T L M T H G S Y R V R I S V L H D	418
1801	ACGGCACGCTTAACCTCACCAACGTCACCGTGCAGGACACGGGCCAGTACACGTGCATGG	1860
419	G T L N F T N V T V Q D T G Q Y T C M V	438
1861	TGACGAACCTCAGCCGGCAACACCACCGCCTCGGCCACGCTCAACGTCTCGGCCGTGGACC	1920
439	T N S A G N T T A S A T L N V S A V D P	458

1921 459	CCGTGGCGGCCCGGGGGCACCGGCAGCGGCGGGGGCGGCCCTGGGGGACAGTGGTGGTGTG	1980 478
1981 479	GAGGGGGACAGTGGCGGCTACACCTACTTCACCACGGTGACCGTGGAGACCCTGGAGACGC	2040 498
2041 499	AGCCCGGAGAGGAGGCCCTGCAGCCGCGGGGACGGAGAAGGAACCGCCAGGGCCCCACGA	2100 518
2101 519	CAGACGGTGTCTGGGGTGGGGGCCGGCCTGGGGACGCGGCCGGCCCTGCCTCGTCTTCTA	2160 538
2161 539	CCACGGCACCCGCCCCGCGCTCCTCGCGGCCACGGAGAAGGCGTTACGGTGCCCATCA	2220 558
2221 559	CGGATGTGACGGAGAACGCCCTCAAGGACCTGGACGACGTCATGAAGACCACAAAATCA	2280 578
2281 579	TCATCGGCTGCTTCGTGGCCATCACGTTTCATGGCCGCGGTGATGCTCGTGGCCTTCTACA	2340 598
2341 599	AGCTGCGCAAGCAGCACCAGCTCCACAAGCACCACGGGCCCCACGCGCACCGTGGAGATCA	2400 618
2401 619	TCAACGTGGAGGACGAGCTGCCCGCCGCTCGGCCGTGTCCGTGGCCGCC	2450 634

Figure 2A

```

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN_PRECURSOR
SLIT-2.
-----MARARGSPCPPLP
-----MLNKMTLHP
MSGIGWQTLSSLALVLSILNKVAPHACPAQCSCSGSTVDCHGLALRIVP

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN_PRECURSOR
SLIT-2.
PGRMSWPHGALLFLWLFSPLGAGGGGVAVTSAAGGGS-PPATSCPVACS
QQIMIGPR----FNRALFDPLLVLVLLALQLLVVAG--L-VRAQTCPSVCS
-----MARPMLLXLXSLGLLASLL----PALAACPNCH
RNIPRNTERLDLNGNNITRITKTDFAGLRHLRILQLMENKISTIERGAFH
.      :      .:

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN_PRECURSOR
SLIT-2.
CSNQASRVICTRRDLAEVPAS---IPVNTRYLNLQENGIQVIRTDTFKHL
CSNQFSKVICVRKNLREVPDG---ISTNTRLLNLHENQIQIIVKNSFKHL
CHSDLQHVICDKVGLQKIPK----VSEKTKLLNLQRNFPVLATNSFRAM
DLKELERLRNLRNNLQFPPELLFLGTAKLYRLDLSENQIQAIIPKAFRGA
.: .: : . * . * . : * : * : : .: :

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN_PRECURSOR
SLIT-2.
RHLEILQLSKNLVRKIEVGAFNGLPSLNTLELFDNRLTTVPTQAFEYLSK
RHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSK
PNLVSLHLQHQCIREVAAGAFRGLKQLIYLYLSHNDIRVLRAFADDLTE
VDIKNLQLDYNQISCIEDGAFRALRDLEVLTLNNNNITRLSVASFNMHPK
.: * : . : : * * . * * * : : : * : :

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN_PRECURSOR
SLIT-2.
LREL-----WLRN-----
LKEL-----WLRN-----
LTYL-----YLDH-----
LRTFRLHSNNLYCDCHLAWLSDWLRQRPRVGLYTQCMGPSHLRGHNVAEV
* : : * :

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN_PRECURSOR
SLIT-2.
-----
-----
-----
QKREFVCSDEEEGHQSFMAPSCSVLHCPIACTCSNNIVDCRGKGLTEIPT

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN_PRECURSOR
SLIT-2.
-----NPIESIPSYAFNRVPSLRRLDLGELKR-----
-----NPIESIPSYAFNRIPSLRRLDLGELKR-----
-----NKVTELPRGLLSPLVNLFILQLNNNK-----
NLPETITEIRLEQNSIRVIPPGAFSPYKKLRRLDLSNNQISELAPDAFQG
* : : * : . * * : :

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN_PRECURSOR
SLIT-2.
-----LEYISEAAFEGLVNLRYNLGMCNLKDIP--NLTAIV
-----LSYISEGAFEGLSNRYNLNLCMLNREIP--NLTPLI
-----IRELRSGAFQGAQDLRWLYLSENSLSLQPGALDDVE
LRSLNSLVLYGNKITELPKSLFEGFLSLQLLLLNANKINCLRVDAFQGLR
: : . * : * : * : : : :

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN_PRECURSOR
SLIT-2.
RLEELELSGNRLDLIRPGSFQGLTSLRKLWLMHAQVATIERNAFDDKSL
KLDELDSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSL
NLAKFYLDNRNLSSYPSAALSCLRVEELKLSHNPLKSIPDNAFQSGFRY
SLNSLVLYGNKITELPKSLFEGFLSLQLLLLNANKINCLRVDAFQDLHNL
* . : * * : . : . * : * : : : : * : :

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN_PRECURSOR
SLIT-2.
EELNLSHN-NLMSLPHDLFTPLHRLERVHLNHNPNWHCNCVDLWLSWWLKE
VEINLAHN-NLTLPHDLFTPLHHLERIHLHNPWNCNCDILWLSWWIKD
LETWLWDNTNLEKFSDBGAFGLVTTLKHVHLENNRLHQLPSNFPDSLET
NLLSLYDN-KLQTVAKGTFALRAIQTMHLAQNPFI CDCHLKLWADLYHT
. * : * . . . * : : : * : * :

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN_PRECURSOR
SLIT-2.
TVPSNTTCCARCHAPAGLKGRYIGELDQSHFTCYAPVIVEPPTDLNVTEG
MAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTG
TLTNNPWKCT-CQLRG-LRWLEAKTSRPDATCASPACFRG----QHIRD
NP--IETSGARCTSPRRLANKRIGQIKSKKFRCSGTEDYRSKLSGDCPAD
. : * * . : . * . . . : .

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN_PRECURSOR
SLIT-2.
MAAELKCRGTGTSMTSVNWLTPNGTLMTHGSYRVRSVLHDGTLNFTNVTV
MAAELKCRATSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTV
TDAFRGCKEPTKRSKKAGR-----
LACPEKCRCEGTTVDCSNQKLNKIPDHIPQYTAELRLN-----NNEFTVL
. * : . . : . : :

```

Figure 2B

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN__PRECURSOR
SLIT-2.

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN__PRECURSOR
SLIT-2.

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN__PRECURSOR
SLIT-2.

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN__PRECURSOR
SLIT-2.

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN__PRECURSOR
SLIT-2.

HLRRNS-1
KIAA1580
BOVIN_CHONDROADHERIN__PRECURSOR
SLIT-2.

QDTGQYTCMVTNSAGNTTASATLNVSADPVAAGGTGSGGGGPGGSGGVG
QDTGMYTCMVNSVGNNTASATLNVT-----AAT-----TT

EATGIFKKLPQLRKINLSNNKITDIEEGAFEGASG-----VN
: : . : .

GGSGGYTYFTTVTVETLETQPGEEALQPRGTEKEPPGPPTDGVWGGGRPG
P----FSYFSTVTVETMEPSQDE----ARTTDNN-VGPTPVVDW-----

EILLTSNRLENVQHMKMFKGLESKTLMLRSNRISCVG-NDSFTGLGSVRL
: : : . .

DAAGPASSSTTAPAPRSSRPTEKAFTVPITDV TEN-ALKDLDDVMKTTKI
----ETNVTTSLTPQSTRSTEKFTTIPVTDINS--GIPGIDEVMKTTKI

LSLYDNQITTVAPGAFGTLHSLSTLNLLANPFNCNCHLAWLGEWLRRKRI
 . : : . .

IIG---CFVAITFMAAVMLVAFYKLRKQHQLHKHHGPTRTVEIINVEDEL
IIG---CFVAITLMAAVMLVIFYKMRKQHHRQNHhapTRTVEIINVDEI

VTGNPRCQKPYFLKEIPIQDVAIQDFTCDDGNDNNSCSPLSRCPSECTCL
:

PAASAVSVAA-----
TGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSSVHEPL

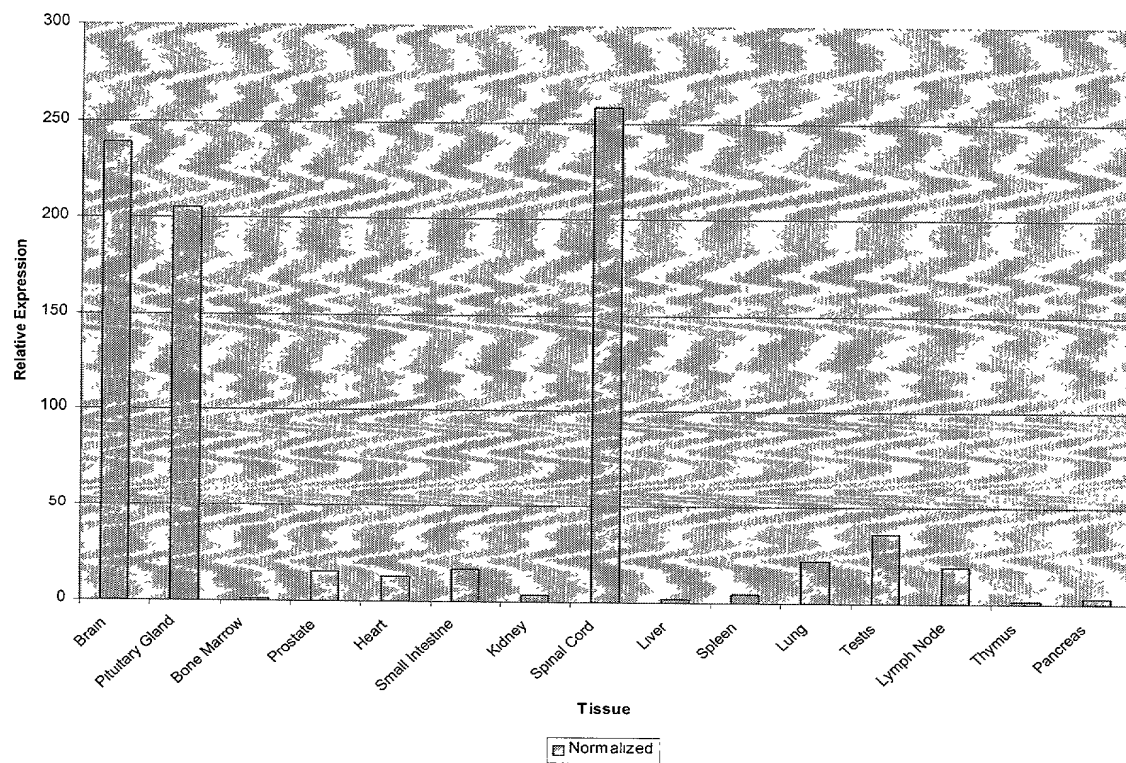
DTVVRC SNKGLKVLPGIPRDVTELYLDGNQFTLVPEFPFFFFFFFSLIF
.

LIRMNSKDNVQETQI-

FLFETGSGGVASALEY

T00E9E1E00I

Figure 3



MARARGSPCPPLPPGRMSWPHGALLFLWLFLSPPLGAGGGGVAVTSAAGGG
MLNKMT-----LHP--QQIMIGPRENRAFDPDLLVL---LAQLLVVAG
-----MARPMLLX-----LSLGLLS-L
-----LALVLSIL-N
-----MSGIGWQTLSSL-----LALVLSIL-N

HLRRNS_1_FL
KIAA1580
BOVIN_CHONDROADHERIN_PRECURSOR
SLIT-2.

SAGNTTASATLNVSAVDPAAGGTGSGGGGPGSGVGSGGGYTYFTTV
 SVGNTTASATLNVTA-----TTT---P-----FSYFSTV

 KRIGQIKSKKFRCSGTEDYRSKLSGDCFADLACPEKCR-CEGTTVDCSNQ

```

TVETLETQPGEEALQPRGTEKEPPGPTTDGVWGGGRPGDAAGPASSSTTA
TVETME--PSQD--EARTTDNN-VGPTPVVDW-----ETTNTVTS
-----
KLNKIPDHIPQYTAE LRLN NNEFTVLEATGIFKKLPQLRKINLSNNKITD
:      .      :      .      :::      .
PAP----RSSRPTEKAFTVPITDVTENALKDLDDVMKTKKII---IGCF-
LTP----QSTRSTEKFTFTIPVTDINS-GIPGIDEVMKTKKII---IGCF-
-----
IEEGAFEGASGVNEILLTSNRLENVQHKMFKGLESKLTMLRSNRNISCVG
:      :      ..      :      :
-VAITFMAAVMLVAFYKLRKQHQHLKHHGPTRTVEIINVEDELPAASAVS
-VAITLMAAVMLVIIFYKMRKQHHRQNHAPTRTVEIINVDDEI---T---
NDSFTGLGSVRLLSLYDNQITTVAPGAFGTLHSLSTLNLNLANPFNCNCHL
.      .      .      :      :
VAAAAAV---ASGGVGVDGSHLALPALERDHLNHHHYVAA-----AFKA
-----GDTPMESHLPMPAIEHEHLNHN-----SYKS
-----
AWLGEWLRRKRIVTGNPRCQKPYFLKEIPIQDVAIQDFTCDGDNDDNSCS
:      .      :      .
HYSSNPSPGGGCGGKGPPLNSIHEPLLFKSGSKENVQETQI-----
PFNHTTTNTIN--SIH--SSVHEPLLIRMNSKDNVQETQI-----
-----
PLSRCPSECTCLD TVVR--CSNKGKLVLPKGI PRDVTELYLDGNQFTLVP
.      .      :      :
-----
-----
-----
EFPFFFFFFFLSIFFLFETSGGVASALEY

```


1	CCACGCGTCCGACTAGTTCTAGATCGCGAGCGGCGCCGCGGGCCCCGAGGAGGGGAGGAAG	60
61	GAAGGAAGGAAGGCTGGAAGGAAGGAAGCCAGGAAAGAAAGAAGGAAAGAAAGGAAGGCA	120
121	AGAAGGAAGGCGGGCGGCGGGGCGAGGGCGCGGGGCCGGACGGCAGGCGGGGCGCGAGGCGA	180
181	GGAGGCAGAGCGGCCCCCCCCAGCCCCACCGCCCGCTGCGGAAGCCCCCTCCCCACCCA	240
241	GGAGCCGGGGAGGGGGGAGAGCGCGAGAGGCTCCAGGCCCGGCCGAGCCCCGCCCCCCCG	300
301	CGCCTCCCCGAGCGGGCCTTGCAACCCCAAATTCCTGAGCCTCATTTGGGGGGGTCTCTCC	360
361	CCCACGGGCGGGGCATGCTGCCCCCGGAAGGAACCCCTCTCCTCGCTCACGATCTCGAC	420
421	AGGAAGCCCTGGAGAACTGGGGAGGCAGAGACCCCGCTGGCCGGAGGCATGTGGAGGGG	480
481	GGGGCCTGGGCGCAGGGAGAGGCCAGCGGAAGCCAAGCCACCAGGCCCCCCCAGCGTCCA	540
541	CGCGGAGCATGAACATTGAGGATGGCGCGTGCCCGCGGCTCCCCGTGCCCCCGCTGCCG	600
1	<u>M A R A R G S P C P P L P</u>	13
601	CCCGGTAGGATGTCCTGGCCCCACGGGGCATTGCTCTTCTCTGGCTCTTCTCCCCACCC	660
14	<u>P G R M S W P H G A L L F L W L F S P P</u>	33
661	CTGGGGGCGGTTGGAGGTGGAGTGGCCGTGACGTCTGCCCGCGGAGGGGGCTCCCCGCCG	720
34	<u>W G A</u> G G G G V A V T S A A G G G S P P	53
721	GCCACCTCCTGCCCCGTGGCCTGCTCCTGCAGCAACCAGGCCAGCCGGGTGATCTGCACA	780
54	A T S C P V A C S C S N Q A S R V I C T	73
781	CGGAGAGACCTGGCCGAGGTCCCAGCCAGCATCCCGGTCAACACGCGGTACCTGAACCTG	840
74	R R D W A E V P A S I P V N T R Y L N W	93
841	CAAGAGAACGGCATCCAGGTGATCCGGACGGACACGTTCAAGCACCTGCGGCACCTGGAG	900
94	Q E N G I Q V I R T D T F K H L R H <u>L</u> E	113
901	ATTCTGCAGCTGAGCAAGAACCTGGTGCGCAAGATCGAGGTGGGCGCCTTCAACGGGCTG	960
114	I W Q L S K N L V R K I E V G A F N G L	133
961	CCCAGCCTCAACACGCTGGAGCTTTTTTGACAACCGGCTGACCACGGTGCCACGCAGGCC	1020
134	P S L N T W E L F D N R L T T V P T Q A	153

Figure 4B

1021	TTCGAGTACCTGTCCAAGCTGCGGGAGCTCTGGCTGCGGAACAACCCCATCGAGAGCATC	1080
154	F E Y <u>L</u> S K <u>L</u> R E <u>L</u> W <u>L</u> R N N P I E S I	173
1081	CCCTCCTACGCCCTTCAACCGCGTGCCTCGCTGCGGCGCCTGGACCTGGGCGAGCTCAAG	1140
174	P S Y A F N R V P S <u>L</u> R R <u>L</u> D <u>L</u> G E L K	193
1141	CGGCTGGAATACATCTCGGAGGCGGCCTTCGAGGGGCTGGTCAACCTGCGCTACCTCAAC	1200
194	R <u>L</u> E Y I S E A A F E G <u>L</u> V N <u>L</u> R Y <u>L</u> N	213
1201	CTGGGCATGTGCAACCTCAAGGACATCCCCAACCTGACGGCCCTGGTGCGCCTGGAGGAG	1260
214	<u>L</u> G M C N <u>L</u> K D I P N <u>L</u> T A <u>L</u> V R <u>L</u> E E	233
1261	CTGGAGCTGTGCGGCAACCGGCTGGACCTGATCCGCCCGGGCTCCTTCCAGGGTCTCACC	1320
234	<u>L</u> E <u>L</u> S G N R <u>L</u> D L I R P G S F Q G <u>L</u> T	253
1321	AGCCTGCGCAAGCTGTGGCTCATGCACGCCAGGTAGCCACCATCGAGCGCAACGCCTTC	1380
254	S <u>L</u> R K <u>L</u> W <u>L</u> M H A Q V A T I E R N A F	273
1381	GACGACCTCAAGTCGCTGGAGGAGCTCAACCTGTCCCACAACAACCTGATGTGCTGCCC	1440
274	D D <u>L</u> K S <u>L</u> E E L N L S H N N <u>L</u> M S <u>L</u> P	293
1441	CACGACCTCTTCACGCCCCTGCACCGCCTCGAGCGCGTGACCTCAACCACAACCCCTGG	1500
294	H D <u>L</u> F T P <u>L</u> H R <u>L</u> E R V H <u>L</u> N H N P W	313
1501	CATTGCAACTGCGACGTGCTCTGGCTGAGCTGGTGGCTCAAGGAGACGGTGCCAGCAAC	1560
314	H C N C D V L W <u>L</u> S W W L K E T V P S N	333
1561	ACGACGTGCTGCGCCCGCTGTCATGCGCCCGCCGGCCTCAAGGGGCGCTACATTGGGGAG	1620
334	T T C C A R C H A P A G <u>L</u> K G R Y I G E	353
1621	CTGGACCAGTCGCATTTACCTGCTATGCGCCCGTCATCGTGGAGCCGCCCACGGACCTC	1680
354	L D Q S H F T C Y A P V I V E P P T D L	373
1681	AACGTCAACGAGGGCATGGCTGCCGAGCTCAAATGCCGCACGGGCACCTCCATGACCTCC	1740
374	N V T E G M A A E L K C R T G T S M T S	393
1741	GTCAACTGGCTGACGCCCCAACGGCACCCCTCATGACCCACGGCTCCTACCGCGTGCGCATC	1800
394	V N W L T P N G T L M T H G S Y R V R I	413
1801	TCCGTCCTGCATGACGGCACGCTTAACCTTACCAACGTACCGTGCAGGACACGGGCCAG	1860
414	S V L H D G T L N F T N V T V Q D T G Q	433
1861	TACACGTGCATGGTGACGAACTCAGCCGGCAACACCACCGCCTCGGCCACGCTCAACGTC	1920
434	Y T C M V T N S A G N T T A S A T L N V	453

Figure 4C

1921	TCGGCCGTGGACCCCGTGGCGGCCCGGGGGCACCGGCAGCGGCGGGGGCGGCCCTGGGGGC	1980
454	S A V D P V A A G G T G S G G G G P G G	473
1981	AGTGGTGGTGTGGAGGGGGCAGTGGCGGCTACACCTACTTCACCACGGTGACCGTGGAG	2040
474	S G G V G G G S G G Y T Y F T T V T V E	493
2041	ACCCTGGAGACGCAGCCCGGAGAGGAGGCCCTGCAGCCGCGGGGGACGGAGAAGGAACCG	2100
494	T L E T Q P G E E A L Q P R G T E K E P	513
2101	CCAGGGCCACGACAGACGGTGTCTGGGGTGGGGGCCGGCCTGGGGACGCGGCCGGCCCT	2160
514	P G P T T D G V W G G G R P G D A A G P	533
2161	GCCTCGTCTTCTACCACGGCACCCGCCCGCGCTCCTCGGGCCACGGAGAAGGCGTTC	2220
534	A S S S T T A P A P R S S R P T E K A F	553
2221	ACGGTGCCCATCACGGATGTGACGGAGAACGCCCTCAAGGACCTGGACGACGTCATGAAG	2280
554	T V P I T D V T E N A L K D L D D V M K	573
2281	ACCACCAAAATCATCATCGGCTGCTTCGTGGCCATCACGTTTCATGGCCGCGGTGATGCTC	2340
574	T T K I I I G C F V A I T F M A A V M L	593
2341	GTGGCCTTCTACAAGCTGCGCAAGCAGCACCAGCTCCACAAGCACCACGGGGCCACGCGC	2400
594	V A F Y K L R K Q H Q L H K H H G P T R	613
2401	ACCGTGGAGATCATCAACGTGGAGGACGAGCTGCCCCGCCCTCGGCCGTGTCCGTGGCC	2460
614	T V E I I N V E D E L P A A S A V S V A	633
2461	GCCGCGGCCGCCGTGGCCAGTGGGGGTGGTGTGGGCGGGGACAGCCACCTGGCCCTGCCC	2520
634	A A A A V A S G G G V G G D S H L A L P	653
2521	GCCCTGGAGCGAGACCACCTCAACCACCACCACTACGTGGCTGCCGCCTTCAAGGCGCAC	2580
654	A L E R D H L N H H H Y V A A A F K A H	673
2581	TACAGCAGCAACCCAGCGGCGGGGGCTGCGGGGGCAAAGGCCCGCTGGCCTCAACTCC	2640
674	Y S S N P S G G G C G G K G P P G L N S	693
2641	ATCCACGAACCTCTGCTCTTCAAGAGCGGCTCCAAGGAGAACGTGCAAGAGACGCAGATC	2700
694	I H E P L L F K S G S K E N V Q E T Q I	713
2701	TGAGGCGGCGGGGCCGGGCGAGGGGCGTGGAGCCCCCACCAGGTCCCAGC	2756

Figure 6.

HLRSI1 (SEQ ID NO:2)

Protein	Genbank ID	Identities	Similarities
bovine chondroadherin precursor	gi 627724	32.3%	37.4%
rat slit-2	gi 6579191	26.7%	33.8%
KIAA1580	gi 10047235	73.9%	65.5%

HLRSI1 (SEQ ID NO:35)

Protein	Genbank ID	Identities	Similarities
bovine chondroadherin precursor	gi 627724	32.3%	37.4%
rat slit-2	gi 6579191	26.7%	33.8%
KIAA1580	gi 10047235	68.0%	75.5%

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